

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 09/980,364A
Source: IFw16
Date Processed by STIC: 7/10/06

ENTERED



IFW16

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/980,364A

DATE: 07/10/2006

TIME: 12:51:55

Input Set : A:\SEQUENCE LISTING.txt

Output Set: N:\CRF4\07102006\I980364A.raw

3 <110> APPLICANT: Boutilier, Kim
 4 Ouellet, Therese
 5 Custers, Jan
 6 Hattori, Jiro
 7 Miki, Brian
 8 Van Lookeren Campagne, Michiel
 10 <120> TITLE OF INVENTION: USE OF THE BNM3 TRANSCRIPTIONAL ACTIVATOR TO CONTROL PLANT
 11 EMBRYOGENESIS AND REGENERATION PROCESSES
 13 <130> FILE REFERENCE: 15327.0001US01
 15 <140> CURRENT APPLICATION NUMBER: 09/980,364A
 16 <141> CURRENT FILING DATE: 2002-04-08
 18 <150> PRIOR APPLICATION NUMBER: PCT/CA00/00642
 19 <151> PRIOR FILING DATE: 2000-06-02
 21 <150> PRIOR APPLICATION NUMBER: EP 99201745.9
 22 <151> PRIOR FILING DATE: 1999-06-02
 24 <160> NUMBER OF SEQ ID NOS: 17
 26 <170> SOFTWARE: PatentIn version 3.3
 28 <210> SEQ ID NO: 1
 29 <211> LENGTH: 2014
 30 <212> TYPE: DNA
 31 <213> ORGANISM: Brassica napus
 33 <400> SEQUENCE: 1
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 40 acgtctactc ttccaccacc acaaccgtcg tagatgtcgc cggagagtgac tgttacgatc 240
 42 cgaccgctgc ctccgatgag ttttccagcca tccaaacatc gtttcttct cccttggtg 300
 44 tcgtcgatc tgctttcacc agagacaaca atagtcactc ccgagatgg gacatcaatg 360
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 48 ttggccgcac caccacgatt tacaacacca acgaaaacgt tggagatgga agtggaaagtg 480
 50 gctgttatgg aggaggagac ggtgggtggtg gctcactagg actttcgatg ataaagacat 540
 52 ggctgagaaa tcaaccgtg gataatgtt ataatacaga aaatggcaat gctgaaaag 600
 54 gcctgtccct ctcaatgaac tcatactactt cttgtataa caacaacgcac agcaataaca 660
 56 acgttgttgc ccaagggaaag actattgtatc atagcgttga agctacaccc aagaaaacta 720
 58 ttgagatgtt tggacagagg acgtctatata accgcgggtgt tacaaggcat cggggacag 780
 60 gaagatatga ggcacattta tggataata gttgtaaaag agaaggccaa acgcgc当地 840
 62 gaagacaagt ttatggatc ggttatgaca aagaagaaaa agcagctagg gcttatgatt 900
 64 tagccgcactt caagtattgg ggaaccacca ctactactaa cttccccatg agcgaatatg 960
 66 aaaaagaggtt agaagagatg aagcacaatgca caaggcaaga gtatgttgc tcactgc当地 1020
 68 ggaaaaagtagt tggtttctct cgtggtgcat cgatttatcg tggagtaaca agacatcacc 1080
 70 aacatggaaat tggcaagctt agataggaa gactgc当地 1140
 72 gaacttttgg cacacaagaa gaagctgcag aggcatcga cattgc当地 1200
 74 gaggattaac cgcagtgactt aacttcgaca tgaacagata caacgttaaa gcaatc当地 1260

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80	ggcaaaacgc	tgcggttcag	catcatcagg	gagtagattt	gagtttattt	caccaacatc	1440									
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86	ctaataatcga	tcatcaaagt	tctgtttcg	atgattcggt	tactgtttgt	ggaardttt	1620									
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119					35			40								45
122	Ser	Ala	Ile	Gln	Thr	Ser	Phe	Pro	Ser	Pro	Phe	Gly	Val	Val	Val	Asp
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131					85			90								95
134	Leu	Glu	Asn	Phe	Leu	Gly	Arg	Thr	Thr	Ile	Tyr	Asn	Thr	Asn	Glu	
135					100			105								110
138	Asn	Val	Gly	Asp	Gly	Ser	Gly	Ser	Gly	Cys	Tyr	Gly	Gly	Gly	Asp	Gly
139					115			120								125
142	Gly	Gly	Gly	Ser	Leu	Gly	Leu	Ser	Met	Ile	Lys	Thr	Trp	Leu	Arg	Asn
143					130			135								140
146	Gln	Pro	Val	Asp	Asn	Val	Asp	Asn	Gln	Glu	Asn	Gly	Asn	Ala	Ala	Lys
147	145				145			150			155					160
150	Gly	Leu	Ser	Leu	Ser	Met	Asn	Ser	Ser	Thr	Ser	Cys	Asp	Asn	Asn	Asn
151										165		170				175
154	Asp	Ser	Asn	Asn	Asn	Val	Val	Ala	Gln	Gly	Lys	Thr	Ile	Asp	Asp	Ser
155										180		185				190
158	Val	Glu	Ala	Thr	Pro	Lys	Lys	Thr	Ile	Glu	Ser	Phe	Gly	Gln	Arg	Thr
159									195		200					205
162	Ser	Ile	Tyr	Arg	Gly	Val	Thr	Arg	His	Arg	Trp	Thr	Gly	Arg	Tyr	Glu
163									210		215					220
166	Ala	His	Leu	Trp	Asp	Asn	Ser	Cys	Lys	Arg	Glu	Gly	Gln	Thr	Arg	Lys
167	225								225		230					240
170	Gly	Arg	Gln	Val	Tyr	Leu	Gly	Gly	Tyr	Asp	Lys	Glu	Glu	Lys	Ala	Ala

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182 His Met Thr Arg Gln Glu Tyr Val Ala Ser Leu Arg Arg Lys Ser Ser
183          290          295          300
186 Gly Phe Ser Arg Gly Ala Ser Ile Tyr Arg Gly Val Thr Arg His His
187 305          310          315          320
190 Gln His Gly Arg Trp Gln Ala Arg Ile Gly Arg Val Ala Gly Asn Lys
191          325          330          335
194 Asp Leu Tyr Leu Gly Thr Phe Gly Thr Gln Glu Glu Ala Ala Glu Ala
195          340          345          350
198 Tyr Asp Ile Ala Ala Ile Lys Phe Arg Gly Leu Thr Ala Val Thr Asn
199          355          360          365
202 Phe Asp Met Asn Arg Tyr Asn Val Lys Ala Ile Leu Glu Ser Pro Ser
203          370          375          380
206 Leu Pro Ile Gly Ser Ala Ala Lys Arg Leu Lys Glu Ala Asn Arg Pro
207 385          390          395          400
210 Val Pro Ser Met Met Ile Ser Asn Asn Val Ser Glu Ser Glu Asn
211          405          410          415
214 Ser Ala Ser Gly Trp Gln Asn Ala Ala Val Gln His His Gln Gly Val
215          420          425          430
218 Asp Leu Ser Leu Leu His Gln His Gln Glu Arg Tyr Asn Gly Tyr Tyr
219          435          440          445
222 Tyr Asn Gly Gly Asn Leu Ser Ser Glu Ser Ala Arg Ala Cys Phe Lys
223          450          455          460
226 Gln Glu Asp Asp Gln His His Phe Leu Ser Asn Thr Gln Ser Leu Met
227 465          470          475          480
230 Thr Asn Ile Asp His Gln Ser Ser Val Ser Asp Asp Ser Val Thr Val
231          485          490          495
234 Cys Gly Asn Val Val Gly Tyr Gly Gly Tyr Gln Gly Phe Ala Ala Pro
235          500          505          510
238 Val Asn Cys Asp Ala Tyr Ala Ala Ser Glu Phe Asp Tyr Asn Ala Arg
239          515          520          525
242 Asn His Tyr Tyr Phe Ala Gln Gln Gln Gln Thr Gln Gln Ser Pro Gly
243          530          535          540
246 Gly Asp Phe Pro Ala Ala Met Thr Asn Asn Val Gly Ser Asn Met Tyr
247 545          550          555          560
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259 <211> LENGTH: 2011
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263 <400> SEQUENCE: 3
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272	atgcttcac	cagagacaac	aatagtcaact	ccc gagattg	ggacatcaat	gttagtgcat	300
274	gtaataacat	ccacaatgtat	gagcaagatg	gacaaaact	tgagaatttc	cttggccgca	360
276	ccaccacgat	ttacaacacc	aacgaaaacg	ttggagatat	cgatggaagt	gggtgttatg	420
278	gaggaggaga	cggtgggtgt	ggctactag	gacttgcgt	gataaagaca	tggctgagaa	480
280	atcaacccgt	ggataatgtt	gataatcaag	aaaatggcaa	tggtgcaaaa	ggctgtccc	540
282	tctcaatgaa	ctcatctact	tcttgtgata	acaacaacta	cagcagtaac	aacctgtttg	600
284	cccaagggaa	gactattgtat	gatagcgttg	aagctacacc	gaagaaaact	attgagagtt	660
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292	tcaagtattt	gggaaccacc	actactacta	acttccccat	gagcgaatat	gagaagagaa	900
294	tagaagagat	gaagcacatg	acaaggcaag	agtatgttc	ctcacttcgc	agggaaaagta	960
296	gtggtttctc	tcgtggtgca	tcgatttata	gtggagtaac	aagacatcac	caacatggaa	1020
298	gatggcaagc	taggatagga	agagtcgccc	gtaacaaaga	cctctacttg	ggaacttttg	1080
300	gcacacaaga	agaagctgca	gaggcataacg	acattgcggc	catcaaattc	agaggattaa	1140
302	cogcagtgac	taacttcgac	atgaacagat	acaacgttaa	agcaatcctc	gaaagcccta	1200
304	gtcttcctat	tggttagcgcc	gcaaaaacgtc	tcaaggaggc	taaccgtccg	gttccaagta	1260
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333 <210> SEQ ID NO: 4

334 <211> LENGTH: 579

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336 <213> ORGANISM: Brassica napus

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345					20				25				30			
348	Val	Ala	Gly	Glu	Tyr	Cys	Tyr	Asp	Pro	Thr	Ala	Ala	Ser	Asp	Glu	Ser
349					35				40				45			
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353					50				55				60			
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376 Gln Pro Val Asp Asn Val Asp Asn Gln Glu Asn Gly Asn Gly Ala Lys
377 145          150          155          160
380 Gly Leu Ser Leu Ser Met Asn Ser Ser Thr Ser Cys Asp Asn Asn Asn
381      165          170          175
384 Tyr Ser Ser Asn Asn Leu Val Ala Gln Gly Lys Thr Ile Asp Asp Ser
385      180          185          190
388 Val Glu Ala Thr Pro Lys Lys Thr Ile Glu Ser Phe Gly Gln Arg Thr
389      195          200          205
392 Ser Ile Tyr Arg Gly Val Thr Arg His Arg Trp Thr Gly Arg Tyr Glu
393      210          215          220
396 Ala His Leu Trp Asp Asn Ser Cys Lys Arg Glu Gly Gln Thr Arg Lys
397 225          230          235          240
400 Gly Arg Gln Val Tyr Leu Gly Gly Tyr Asp Lys Glu Glu Lys Ala Ala
401      245          250          255
404 Arg Ala Tyr Asp Leu Ala Ala Leu Lys Tyr Trp Gly Thr Thr Thr
405      260          265          270
408 Thr Asn Phe Pro Met Ser Glu Tyr Glu Lys Glu Ile Glu Glu Met Lys
409      275          280          285
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413      290          295          300
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417 305          310          315          320
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421      325          330          335
424 Asp Leu Tyr Leu Gly Thr Phe Gly Thr Gln Glu Ala Ala Glu Ala
425      340          345          350
428 Tyr Asp Ile Ala Ala Ile Lys Phe Arg Gly Leu Thr Ala Val Thr Asn
429      355          360          365
432 Phe Asp Met Asn Arg Tyr Asn Val Lys Ala Ile Leu Glu Ser Pro Ser
433      370          375          380
436 Leu Pro Ile Gly Ser Ala Ala Lys Arg Leu Lys Glu Ala Asn Arg Pro
437 385          390          395          400
440 Val Pro Ser Met Met Ile Ser Asn Asn Val Ser Glu Ser Glu Asn
441      405          410          415
444 Asn Ala Ser Gly Trp Gln Asn Ala Ala Val Gln His His Gln Gly Val
445      420          425          430
448 Asp Leu Ser Leu Leu Gln Gln His Gln Glu Arg Tyr Asn Gly Tyr Tyr
449      435          440          445
452 Tyr Asn Gly Gly Asn Leu Ser Ser Glu Ser Ala Arg Ala Cys Phe Lys
453      450          455          460
456 Gln Glu Asp Asp Gln His His Phe Leu Ser Asn Thr Gln Ser Leu Met
457 465          470          475          480
460 Thr Asn Ile Asp His Gln Ser Ser Val Ser Asp Asp Ser Val Thr Val

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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:8,9,10,11,12,13,14

VERIFICATION SUMMARY

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